

SEQUENCE LISTING

<110> Sode, Koji

<120> GLUCOSE DEHYDROGENASE/CYTOCHROME FUSION PROTEIN

<130> 3691-0130PUS1

<140> US 10/574,085

<141> 2006-03-30

<150> PCT/JP2004/014575

<151> 2004-09-28

<150> JP 2003-340092

<151> 2003-09-30

<160> 6

<170> PatentIn version 3.1

<210> 1

<211> 1776

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA coding for a fusion protein

<400> 1

atgaataaaac	atttatttggc	taaaaattgct	ttattaagcg	ctgttcagct	agttacactc	60
tcagcatttgc	ctgatgttcc	tctaactcca	tctcaatttg	ctaaagcgaa	atcagagaac	120
tttgcacaaga	aagtatttct	atctaattcta	aataagccgc	atgctttgtt	atggggacca	180
gataatcaaa	tttggtaaac	tgagcgagca	acaggttaga	ttcttaagagt	taatccagag	240
tcgggtatgt	taaaaaacagt	ttttcaggta	ccagagattt	tcaatgtatc	tgatgggcag	300
aatggtttat	taggtttgc	cttccatcct	gattttaaaa	ataatccta	tatctatatt	360
tcaggtacat	ttaaaaatcc	gaaatctaca	gataaagaat	taccgaacca	aacgattatt	420
cgtcggtata	cctataataa	atcaacagat	acgctcgaga	agccagtctg	tttatttagca	480
ggattacctt	catcaaaaga	ccatcagtca	ggtcgtctt	tcattggccc	agatcaaaag	540
atttatttata	cgattggtga	ccaagggcgt	aaccagctt	cttattttgtt	cttgc当地at	600
caagcacaac	atacgccaac	tcaacaagaa	ctgaatggta	aagactatca	cacctataatg	660
ggtaaagtac	tacgcttaaa	tcttgcgttga	agtattccaa	aggataatcc	aagttttaac	720
gggggtgttta	gccatattta	tacacttggc	catcgtaatc	cgcaggcgtt	agcatttact	780
ccaaatggta	aattatttgc	gtctgaacaa	ggcccaaact	ctgacgtatc	aattaacctc	840
attgtcaaaag	gtggcaattt	tgggtggccg	aatgtacgt	gttataaaga	tgatagtggc	900
tatgctttag	caaatttattc	agcagcagcc	aataagtcaa	ttaaggattt	agctcaaaat	960
ggagtaaaag	tagccgcagg	ggtccctgtt	acgaaaagaat	ctgaatggac	tggtaaaaac	1020
tttgtccac	cattaaaaac	tttatatacc	gttcaagata	cctacaacta	taacgatcca	1080
acttgtggag	agatgaccta	catttgcgtt	ccaacagtt	caccgtcatc	tgccttatgtc	1140
tataaggcgc	gtaaaaaaaa	aattacttgg	tggaaaata	cattattgtt	tccatcttta	1200
aaacgtggtg	tcattttccg	tattaagtta	gatccaactt	atagcactac	ttatgtatgc	1260
gctgtaccga	tgtttaagag	caacaaccgt	tatcgatgt	tgatttgcag	tccagatggg	1320
aatgtcttat	atgttataac	tgataacttgc	ggaaatgtcc	aaaaagatgt	tggctcagta	1380
acaatatacat	tagaaaaaccc	aggatcttcc	attaagtca	cctataaggc	taaggagctc	1440
ggcaaggcca	ggatgcccga	gttcgtggcc	cagcgaccgc	gccagttgt	gcaggcgtg	1500
aaatacgacc	ccgccaaggt	cgaggccggc	accatgtgt	atgtggccaa	ctgcgtttc	1560
tgtcacggcg	tgccctggcgt	ggaccgtggc	ggaaacattc	ccaatctgg	ttacatggac	1620

gcgagctata tcgagaacct gccaaacttt gtcttcaagg gcccggccat ggtgcgcggc 1680
atgccggact tcacggcaa gttgtcgggc gatgacgtgg agtccctcaa ggccttcata 1740
cagggcacgg cggacgcccatt ccctga 1776

<210> 2
<211> 591
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic fusion protein

<400> 2
Met Asn Lys His Leu Leu Ala Lys Ile Ala Leu Leu Ser Ala Val Gln
1. 5 10 15
Leu Val Thr Leu Ser Ala Phe Ala Asp Val Pro Leu Thr Pro Ser Gln
20 25 30
Phe Ala Lys Ala Lys Ser Glu Asn Phe Asp Lys Lys Val Ile Leu Ser
35 40 45
Asn Leu Asn Lys Pro His Ala Leu Leu Trp Gly Pro Asp Asn Gln Ile
50 55 60
Trp Leu Thr Glu Arg Ala Thr Gly Lys Ile Leu Arg Val Asn Pro Glu
65 70 75 80
Ser Gly Ser Val Lys Thr Val Phe Gln Val Pro Glu Ile Val Asn Asp
85 90 95
Ala Asp Gly Gln Asn Gly Leu Leu Gly Phe Ala Phe His Pro Asp Phe
100 105 110
Lys Asn Asn Pro Tyr Ile Tyr Ile Ser Gly Thr Phe Lys Asn Pro Lys
115 120 125
Ser Thr Asp Lys Glu Leu Pro Asn Gln Thr Ile Ile Arg Arg Tyr Thr
130 135 140
Tyr Asn Lys Ser Thr Asp Thr Leu Glu Lys Pro Val Asp Leu Leu Ala
145 150 155 160
Gly Leu Pro Ser Ser Lys Asp His Gln Ser Gly Arg Leu Val Ile Gly
165 170 175
Pro Asp Gln Lys Ile Tyr Tyr Thr Ile Gly Asp Gln Gly Arg Asn Gln
180 185 190
Leu Ala Tyr Leu Phe Leu Pro Asn Gln Ala Gln His Thr Pro Thr Gln
195 200 205
Gln Glu Leu Asn Gly Lys Asp Tyr His Thr Tyr Met Gly Lys Val Leu
210 215 220
Arg Leu Asn Leu Asp Gly Ser Ile Pro Lys Asp Asn Pro Ser Phe Asn
225 230 235 240
Gly Val Val Ser His Ile Tyr Thr Leu Gly His Arg Asn Pro Gln Gly
245 250 255
Leu Ala Phe Thr Pro Asn Gly Lys Leu Leu Gln Ser Glu Gln Gly Pro
260 265 270
Asn Ser Asp Asp Glu Ile Asn Leu Ile Val Lys Gly Asn Tyr Gly
275 280 285
Trp Pro Asn Val Ala Gly Tyr Lys Asp Asp Ser Gly Tyr Ala Tyr Ala
290 295 300
Asn Tyr Ser Ala Ala Ala Asn Lys Ser Ile Lys Asp Leu Ala Gln Asn
305 310 315 320
Gly Val Lys Val Ala Ala Gly Val Pro Val Thr Lys Glu Ser Glu Trp
325 330 335
Thr Gly Lys Asn Phe Val Pro Pro Leu Lys Thr Leu Tyr Thr Val Gln

	340	345	350
Asp Thr Tyr Asn Tyr Asn Asp Pro Thr Cys Gly Glu Met Thr Tyr Ile	355	360	365
Cys Trp Pro Thr Val Ala Pro Ser Ser Ala Tyr Val Tyr Lys Gly Gly	370	375	380
Lys Lys Ala Ile Thr Gly Trp Glu Asn Thr Leu Leu Val Pro Ser Leu	385	390	395
Lys Arg Gly Val Ile Phe Arg Ile Lys Leu Asp Pro Thr Tyr Ser Thr	405	410	415
Thr Tyr Asp Asp Ala Val Pro Met Phe Lys Ser Asn Asn Arg Tyr Arg	420	425	430
Asp Val Ile Ala Ser Pro Asp Gly Asn Val Leu Tyr Val Leu Thr Asp	435	440	445
Thr Ala Gly Asn Val Gln Lys Asp Asp Gly Ser Val Thr Asn Thr Leu	450	455	460
Glu Asn Pro Gly Ser Leu Ile Lys Phe Thr Tyr Lys Ala Lys Glu Leu	465	470	475
Gly Lys Ala Arg Met Pro Glu Phe Val Ala Gln Arg Thr Gly Gln Leu	485	490	495
Leu Gln Gly Val Lys Tyr Asp Pro Ala Lys Val Glu Ala Gly Thr Met	500	505	510
Leu Tyr Val Ala Asn Cys Val Phe Cys His Gly Val Pro Gly Val Asp	515	520	525
Arg Gly Gly Asn Ile Pro Asn Leu Gly Tyr Met Asp Ala Ser Tyr Ile	530	535	540
Glu Asn Leu Pro Asn Phe Val Phe Lys Gly Pro Ala Met Val Arg Gly	545	550	555
Met Pro Asp Phe Thr Gly Lys Leu Ser Gly Asp Asp Val Glu Ser Leu	565	570	575
Lys Ala Phe Ile Gln Gly Thr Ala Asp Ala Ile Arg Pro Lys Pro	580	585	590

<210> 3
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 3
 ggccatggat aaacatttat tggctaaaat tgctttat

38

<210> 4
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 4
 gggggagctc ctaggcctta taggtgaac

29

<210> 5
 <211> 30
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 5

gggggagctc ggcaaggcca ggatgccgga

30

<210> 6

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 6

gggaaagctt tcagggcttg ggccggatgg

30